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GbMYBR1      --EIRAS-----RIFLPSFRGNQVSSHSEL-----MAPA
Pt_AtMYB3-like2  --CSSAS-----EKTRETHPDFMFP-----HPVA
Pt_AtMYB3-like7  SIPLSHQ-----ESFCEYLQKKPLCEH-----FTGI
AtMYB3       -----EDWVLNLEISVGPSYR-----YEST
Pt_AtMYB3-like5  --TEATN-----CTSSMLNFGDQQSPYSDFEGDAANLAESL
Pt_AtMYB3-like3  GMRLAPAKIGGTSISAGVPAPVSSDEVINMKSWKQLLEDLSLMSDFDSEDDTSLMGIELS
Pt_AtMYB3-like6  --EKDAS-----ETWCQLLEDCTGYL-----YDRL
Pt_AtMYB3-like1  --EIDTS-----KSWLQILLEDCMGEYH-----YNLL
Pt_AtMYB3-like4  --EIDTS-----KSWCQLLEDCTGDYQ-----YDRL

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EAR – suppression domain

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GbMYBR1      N-----PMIESNIDRKLFLSLVDDYLSVSTELSLGFSGMNCVSKFS---TNSHNL---
Pt_AtMYB3-like2  S-----SDAGKQTNDSVYCSSDSAASC SLIEHFSEDDHHYLSMEGN-SNECYSQTL
Pt_AtMYB3-like7  D-----INNDNKTDGGSNVGDPNLLIPSSFHDPIFSDKHCNYSSTHSI-SNEISSHG
AtMYB3       R-----KVSVD SAESTRRWG-----SELFGAHESDAVCLCCRIGLFRNESCRN---
Pt_AtMYB3-like5  L-----FLTDLSSPCNLLASPCDSTDFASEDLYRGAALPEETNGF-EDMCSQNN
Pt_AtMYB3-like3  DDVLGSEAPLMEIQTNVSCSTSGPNEPVHSHGHLLADATSNQRSSSENVLYSQDCNVLSL
Pt_AtMYB3-like6  E-----FVQGLQTDRI-----NLLPPSVSPSGSEILQEKQ---SSCNL---
Pt_AtMYB3-like1  Q-----PNIMTNTKCGTDY-----DNQFPSPPTLGRDILLQENG---ASSCNF---
Pt_AtMYB3-like4  E-----EISGLQPNMSMTNSSNVTDQHQHQQPSPFVVSQSIILQENH---SSCDL---

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GbMYBR1      -----YLMGSSLSNTDHHM-----PCGDQSV
Pt_AtMYB3-like2  AEDYGS LKPSTPHTESEPI CDSRERDNDSHVQKHDQFPEYDVFSFFDV---RNAENEIC
Pt_AtMYB3-like7  LGSEISSHVLDLNTDLLQYYLSEG---PCEPAVCS ELAPEDQSSIANLGSGKDYWNDILK
AtMYB3       -----CRVSDVRTH-----
Pt_AtMYB3-like5  MQRVNSSMMDQELEGFYNNAQDEDWIHELDCLENSGAQP-----LSSLLL
Pt_AtMYB3-like3  PPTDNTLDFRIQDFSLESLLLPSVYNFDEICPVQSQLNSSDHVSCFAVAEQAMTDIYNN
Pt_AtMYB3-like6  -----LEEEFLQ TENFNS-----TYF-----
Pt_AtMYB3-like1  -----FDQEFPHSKEFIS-----PYS DNCLD
Pt_AtMYB3-like4  -----IQQESPHSKDFIS-----SYFSSFLD

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GbMYBR1      RDQYRWMNT-----
Pt_AtMYB3-like2  CSADQWVHEQEAEFMQQKQDEMAQLGSWEKQIDDQEKENFESHVNNVDVTAMSWEASF WF-
Pt_AtMYB3-like7  MVNSSSSVDNIF-----
AtMYB3       -----
Pt_AtMYB3-like5  ESEDEWEERSIGKLALEDHVQI-----
Pt_AtMYB3-like3  TLEPDWLT PVEYEKQSTQSDQMNLGNFFLSEENWEEVPTSLSKIQEEYRAILVDISN
Pt_AtMYB3-like6  -----
Pt_AtMYB3-like1  LGEPSFVIP-----
Pt_AtMYB3-like4  LGEQSILLP-----

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GbMYBR1      -
Pt_AtMYB3-like2  -
Pt_AtMYB3-like7  -
AtMYB3       -
Pt_AtMYB3-like5  -
Pt_AtMYB3-like3  K
Pt_AtMYB3-like6  -
Pt_AtMYB3-like1  -
Pt_AtMYB3-like4  -

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R2 – DNA binding domain is highlighted in yellow.

R3 – DNA binding domain is highlighted in green.

bHLH binding motif – Indicated by red box.

C1 motif – Highlighted in pink.

EAR – Suppression domain is highlighted in light blue (which comprises part of the C2 motif).

Alternative EAR domain in Pt_AtMYB4-like1, Pt_AtMYB4-like3, Pt_AtMYB4-like4 and Pa_AtMYB4-like1 are marked with box and, bold and underlined.

Zinc-finger motif – Highlighted in dark blue (C3 motif).

C4 motif – Highlighted in grey. The **GY/FDFLGI** motif is indicated by black box.